

- 1 -

piece 1, NC\_000913, rrfe\_yjaA-, config: linear, direction: -, begin: 4211286, end: 4211163

ir rrfE\_yja

```
sd-(15)-ir 4211241 Gap 6.0 bits  
sd-ir 4211241 rrfE_yjaA- total 8.2 bits
```

The diagram illustrates the sequence alignment between the top strand (5' to 3') and the bottom strand (3' to 5'). The top strand is labeled with positions \* 42111200 \*, \* 42111190 \*, \* 42111180 \*, \* 42111170 \*, and ends with a stop sign (\*). The bottom strand shows the amino acid sequence: trp - thr - gly - val - phe - leu - ile -. A red circle highlights the third position of the first codon (gly), which is preceded by a stop sign (\*). Below the sequence, the codons are explicitly listed: - asp - arg - gly - phe - ser - asn - leu - met - pro - gly - ser - ser - leu -. A bracket below the sequence indicates the reading frame shift at codon 20, spanning from the start of the second codon to the end of the fifth codon.